

OM protein - protein search, using sw model

Run on: April 29, 2004, 10:41:53 ; Search time 54 Seconds
(without alignments)
423.821 Million cell updates/sec

Title: US-09-856-840C-2

Perfect score: 473
Sequence: 1 MFLVFLCCLHLVISHPTD.....VEMVYSTGQCRTTCPTVG 81

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

- Database :
- 1: Genesegp294n04:*
 - 2: Genesegp1980s:*
 - 3: Genesegp2000s:*
 - 4: Genesegp2001s:*
 - 5: Genesegp2002s:*
 - 6: Genesegp2003as:*
 - 7: Genesegp2003bs:*
 - 8: Genesegp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	453	95.8	81	3 AAY92938	Aay92938 Hirudo me
2	79	16.7	145	4 AAM87649	Aam87649 Human imm
3	76	16.1	19938	6 ABP76678	Abp76678 Streptomy
4	75.5	16.0	355	5 ABP69588	Abp69588 Human pol
5	75.5	16.0	355	5 AAU97101	Aau97101 Human MK6
6	75.5	16.0	355	7 ADC37275	Adc37275 Nuclea f
7	75.5	16.0	380	5 AAU97114	Aau97114 Human MK6
8	75	15.9	294	5 ABP95622	Abp95622 Human GPC
9	74.5	15.8	136	5 AAU97103	Aau97103 Human MK6

ALIGNMENTS

RESULT 1		AAY92938 standard; protein, 81 AA.	
XX	XX	ID	AAY92938
XX	AC	AY92938:	
XX	DT	08-NOV-2000 (first entry)	
XX	DE	Hirudo medicinalis metalloproteinase inhibitor protein.	
XX	KW	Recombinant; leech; metalloproteinase inhibitor; fibrin;	
KW	KW	plasma carboxypeptidase B; fibrinolysis inhibitor; plasminogen;	
XX	OS	blood clot.	
XX	XX	Hirudo medicinalis.	

10	73.5	15.5	105	7 ADC31222	Adc31222 Human nov
11	73	15.4	515	2 AAR48670	Aar48670 Chitinase
12	72	15.2	1083	4 ABB60057	Abb60057 Drosophi
13	71.5	15.1	56	4 AAM37769	Aam37769 Peptide #
14	71.5	15.1	56	4 AAM77584	Aam77584 Human bon
15	71.5	15.1	56	4 AAM64835	Aam64835 Human bra
16	71.5	15.1	56	4 AAG59231	Aag59231 Human liv
17	71.5	15.1	85	5 AAU97102	Aau97102 Human MK6
18	71.5	15.1	113	4 ABE30035	Ab30035 Novel hum
19	71	15.0	761	4 ABB60973	Abb60973 Drosophi
20	68.5	14.5	82	4 AAU57028	Aau57028 Propionib
21	68.5	14.5	82	6 ABE53547	Ab53547 Propionib
22	68.5	14.5	727	2 AAR05533	Aar05533 Firmic
23	68.5	14.5	1214	3 AAY79152	Aay79152 Mouse pro
24	68.5	14.5	19938	6 ABE86398	Abb86398 Streptomy
25	68	14.4	100	2 AAM48795	Aam48795 Homo sapi
26	68	14.4	197	4 ABE12460	Ab12460 Human bon
27	68	14.4	288	4 ABE12377	Ab12377 Human bon
28	68	14.4	288	6 AB007186	Ab007186 Human p53
29	68	14.4	934	5 AAU72893	Aau72893 Human met
30	68	14.4	1964	2 AAM95557	Aam95557 Mus muscu
31	67.5	14.3	74	4 AA010231	Aa010231 Human pol
32	67.5	14.3	325	3 AAG60058	Aag60058 Atrichops
33	67.5	14.3	548	7 ADC87345	Adc87345 Human GPC
34	67.5	14.3	1872	2 AAM68510	Aam68510 Partial h
35	67.5	14.3	2321	2 AAY49698	Aay49698 Human Not
36	67	14.2	227	2 AAY17648	Aay17648 Human put
37	67	14.2	227	6 ADB17578	Adb17578 Amino aci
38	67	14.2	228	2 AAY17679	Aay17679 Human WIS
39	67	14.2	228	6 ADB17636	Adb17636 Human WIS
40	67	14.2	229	2 AAY17678	Aay17678 Human WIS
41	67	14.2	229	6 ADB17635	Adb17635 Human WIS
42	67	14.2	230	2 AAY17677	Aay17677 Human WIS
43	67	14.2	230	6 ADB17634	Adb17634 Human WIS
44	67	14.2	231	2 AAY17676	Aay17676 Human WIS
45	67	14.2	231	6 ADB17633	Adb17633 Human WIS

Key Location/Qualifiers
 FT Peptide 1..15
 FT /note="signal peptide"
 FT Protein 16..81
 FT /note="mature metalloproteinase inhibitor"
 XX
 XX WC200001140-A1.
 XX
 XX 02-JUN-2000.
 XX
 XX 24-NOV-1999; 99MO-ES000378.
 XX
 XX 25-NOV-1998; 98ES-00002524.
 XX
 XX (UYBA-) UNIV AUTONOMA BARCELONA.
 XX (UYMU-) UNIV MUENCHEN MAXIMILIANS LUDWIG.
 XX
 XX Reverte D, Vendrell J, Canals F, Horstmann U, Querol E, Fritz H,
 PI Sommerhoff CP, Aviles FX;
 XX
 XX WPI; 2000-40047/34.
 DR N-PSDB; AAA11268.
 XX
 XX New recombinant nucleic acid encoding metalloproteinase inhibitor,
 PT useful as fibrinolytic agent, is derived from the leech Hirudo
 PT medicinalis.
 XX
 XX Claim 3; Page 17; 21pp; Spanish.
 XX
 XX This sequence represents a protein derived from Hirudo medicinalis
 CC (leeches) that inhibits metalloproteinases, particularly of plasma
 CC carboxypeptidase B which inhibits fibrinolysis by destroying the binding
 CC site, in plasminogen, for fibrin. The inhibitor is useful as a
 CC fibrinolytic agent, thus promotes activity of plasminogen and speeds up
 CC lysis of blood clots
 XX
 XX Sequence 81 AA:
 SQ
 Query Match 55.8%; Score 453; DB 3; Length 81;
 Best Local Similarity 97.5%; Pred. No. 2.1e-39;
 Matches 78; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 OY 1 MFLVFLCCLHLVISHPTDESFLCTQPDVCCFCIGGAAPLPSGECNPHPTAPWCRES 60
 DB 1 MFLVFLCCLHLVISHPTDESFLCTQPDVCCFCIGGAAPLPSGECNPHPTAPWCRES 60
 OY 61 AVEWVYSTGQCRTTCIPYV 80
 DB 61 AVEWVYSTGQCRTTCIPYV 80
 Search completed: April 29, 2004, 10:48:46
 Job time : 57 secs

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OM protein - Protein search, using sw model

Run on: April 29, 2004, 10:50:09; Search time 42 seconds
 (without alignments)
 534,580 Million cell updates/sec

Title: US-09-856-840C-2
 Perfect score: 473
 Sequence: 1 MFLVFLCCLHLVISHPTD.....VEWVYSTGQCRTTCIPYV 81

Scoring table: BLOSUM62
 Gapop 10.0, Gapext 0.5

Searched: 1138120 seqs, 277189581 residues
 Total number of hits satisfying chosen parameters: 1138120

Minimum DB seq length: 0
 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database: Published Applications AA:
 1: /cgn2_6/prodata/2/pubppaa/US07_PUBCOMB.pep.*
 2: /cgn2_6/prodata/2/pubppaa/ECT_NEW_PUB.pep.*
 3: /cgn2_6/prodata/2/pubppaa/US06_NEW_PUB.pep.*
 4: /cgn2_6/prodata/2/pubppaa/US06_PUBCOMB.pep.*
 5: /cgn2_6/prodata/2/pubppaa/US07_NEW_PUB.pep.*
 6: /cgn2_6/prodata/2/pubppaa/ECTUS_PUBCOMB.pep.*
 7: /cgn2_6/prodata/2/pubppaa/US08_NEW_PUB.pep.*
 8: /cgn2_6/prodata/2/pubppaa/US08_PUBCOMB.pep.*
 9: /cgn2_6/prodata/2/pubppaa/US09A_PUBCOMB.pep.*
 10: /cgn2_6/prodata/2/pubppaa/US09C_PUBCOMB.pep.*
 11: /cgn2_6/prodata/2/pubppaa/US09C_PUBCOMB.pep.*
 12: /cgn2_6/prodata/2/pubppaa/US09_NEW_PUB.pep.*
 13: /cgn2_6/prodata/2/pubppaa/US10A_PUBCOMB.pep.*
 14: /cgn2_6/prodata/2/pubppaa/US10B_PUBCOMB.pep.*
 15: /cgn2_6/prodata/2/pubppaa/US10C_PUBCOMB.pep.*
 16: /cgn2_6/prodata/2/pubppaa/US10_NEW_PUB.pep.*
 17: /cgn2_6/prodata/2/pubppaa/US60_NEW_PUB.pep.*
 18: /cgn2_6/prodata/2/pubppaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
------------	-------	-------------	--------	----	-------------

1	75.5	16.0	355	9	US-09-948-018-2	Sequence 2, Appl1
2	75.5	16.0	380	9	US-09-948-018-36	Sequence 36, Appl1
3	75.5	15.9	294	12	US-10-343-650A-54	Sequence 54, Appl1
4	74.5	15.8	136	9	US-09-948-018-6	Sequence 6, Appl1
5	73.5	15.5	485	14	US-10-184-544-185	Sequence 185, App
6	73.5	15.5	485	14	US-10-184-534-185	Sequence 185, App
7	73.5	15.5	485	14	US-10-063-685-43	Sequence 43, Appl
8	71.5	15.1	56	9	US-09-864-761-46095	Sequence 46095, A
9	71.5	15.1	85	9	US-09-948-018-4	Sequence 4, Appl1
10	71.5	15.0	19725	15	US-10-084-845A-4	Sequence 4, Appl1
11	68.5	14.5	4660	16	US-10-464-368-74	Sequence 74, Appl1
12	68.5	14.5	19685	15	US-10-084-846A-3	Sequence 3, Appl1
13	68	14.4	455	12	US-10-424-599-221866	Sequence 221866,
14	68	14.4	934	12	US-10-275-107-53	Sequence 53, Appl
15	67.5	14.3	548	14	US-10-017-161-2152	Sequence 2152, Ap
16	67.5	14.3	548	15	US-10-292-798-1798	Sequence 1798, Ap
17	67.5	14.3	1955	12	US-10-072-012-793	Sequence 793, App
18	67.5	14.3	2321	14	US-10-356-625-2	Sequence 2, Appl1
19	67	14.2	202	9	US-09-729-835-90	Sequence 90, Appl
20	67	14.2	202	16	US-10-373-809-90	Sequence 15, Appl
21	67	14.2	227	14	US-10-112-267-15	Sequence 77, Appl
22	67	14.2	228	14	US-10-112-267-77	Sequence 76, Appl
23	67	14.2	229	14	US-10-112-267-76	Sequence 75, Appl
24	67	14.2	230	14	US-10-112-267-75	Sequence 74, Appl
25	67	14.2	231	14	US-10-112-267-74	Sequence 73, Appl
26	67	14.2	232	14	US-10-112-267-73	Sequence 72, Appl
27	67	14.2	233	14	US-10-112-267-72	Sequence 71, Appl
28	67	14.2	234	14	US-10-112-267-71	Sequence 70, Appl
29	67	14.2	235	14	US-10-112-267-70	Sequence 69, Appl
30	67	14.2	236	14	US-10-112-267-69	Sequence 68, Appl
31	67	14.2	237	14	US-10-112-267-68	Sequence 67, Appl
32	67	14.2	238	14	US-10-112-267-67	Sequence 66, Appl
33	67	14.2	239	14	US-10-112-267-66	Sequence 65, Appl
34	67	14.2	240	14	US-10-112-267-65	Sequence 64, Appl
35	67	14.2	241	14	US-10-112-267-64	Sequence 63, Appl
36	67	14.2	242	14	US-10-112-267-63	Sequence 62, Appl
37	67	14.2	243	14	US-10-112-267-62	Sequence 61, Appl
38	67	14.2	244	14	US-10-112-267-61	Sequence 60, Appl
39	67	14.2	245	14	US-10-112-267-60	Sequence 59, Appl
40	67	14.2	246	14	US-10-112-267-59	Sequence 58, Appl
41	67	14.2	247	14	US-10-112-267-58	Sequence 57, Appl
42	67	14.2	248	14	US-10-112-267-57	Sequence 56, Appl
43	67	14.2	249	14	US-09-915-582-53	Sequence 53, Appl
44	67	14.2	250	9	US-09-915-582-53	Sequence 69, Appl
45	67	14.2	250	9	US-09-915-582-69	Sequence 69, Appl

Search completed: April 29, 2004, 10:55:50
Job time : 42 secs

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OM protein - protein search, using sw model

Run on: April 29, 2004, 10:46:48 ; Search time 20 Seconds
(without alignments)
389.576 Million cell updates/sec

Title: US-09-956-840C-2
Perfect score: 473
Sequence: 1 MFLVFLCCLHLVLSHTPD.....VEMVPYSTGQCRTTCPTVG 81

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues
Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: p1r1.*
2: p1r2.*
3: p1r3.*
4: p1r4.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	77	16.3	572	2	T29880
2	72	15.2	335	2	T31559
3	72	15.2	1106	2	T44598
4	71.5	15.1	407	2	S44909
5	71	15.0	1106	2	T13938
6	70	14.8	335	2	T31560
7	70	14.8	335	2	T31561
8	70	14.8	348	2	S09273
9	68.5	14.5	4660	2	T42737
10	68	14.4	345	2	T25138
11	68	14.4	358	2	T25137
12	68	14.4	417	2	A54416
13	68	14.4	813	2	T21192

hypothetical prote
hypothetical prote
hypothetical prote
2K686.4 protein -
gene shuttle craft
hypothetical prote
hypothetical prote
Ig alpha chain C r
sp330 protein prec
hypothetical prote
hypothetical prote
proteasycln recep
hypothetical prote

14	68	14.4	1964	2	T09059
15	68	14.4	3175	1	REWEV
16	67.5	14.3	869	1	UC4858
17	67.5	14.3	1955	1	AGCH
18	67.5	14.3	2321	2	S78549
19	67	14.2	211	2	B89716
20	67	14.2	241	2	T22216
21	67	14.2	400	2	S35528
22	67	14.2	548	2	T25401
23	66.5	14.1	1959	1	AGRT
24	65	13.7	435	2	AD1955
25	65	13.7	488	2	A48203
26	65	13.7	854	1	Q8HYLD
27	65	13.7	1945	2	T13937
28	65	13.7	2643	2	T29149
29	64.5	13.6	158	2	T07597
30	64	13.5	103	1	T1SYC2
31	64	13.5	388	2	A88949
32	64	13.5	444	2	B83802
33	63.5	13.4	153	1	XP0C1
34	63.5	13.4	226	2	J02070
35	63.5	13.4	972	2	A30363
36	63.5	13.4	1063	1	GNMVA
37	63.5	13.4	1319	2	S49951
38	63.5	13.4	2533	2	T28675
39	63.5	13.4	2533	2	T28674
40	63.5	13.4	2555	2	A40043
41	63.5	13.4	4545	1	S25111
42	63	13.3	120	2	A48837
43	63	13.3	124	1	T1BHB
44	63	13.3	157	2	B48837
45	63	13.3	309	2	B87576

Search completed: April 29, 2004, 10:50:36
Job time : 21 secs

notch4 - mouse
genome polyprotein
VLDL receptor prec
agrin precursor -
notch3 protein - h
protein F458.3 (1
hypothetical prote
surface antigen -
hypothetical prote
agrin - rat
two-component sens
interleukin-14 pre
LDL receptor precu
plexin A - fruit f
hypothetical prote
proteinase inhibit
protein R0985.5 (1
hypothetical prote
proteinase inhibit
surface antigen -
glycoprotein GP330
structural polypep
SMA protein - yes
alpha-5ID immunobi
alpha-5ID-immobili
notch protein homo
alpha-2-macroglobu
subgroup A Rous sa
trypsin inhibitor
subgroup A Rous sa
hypothetical prote

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OM protein - protein search, using sw model

Run on: April 29, 2004, 10:43:18 ; Search time 14 seconds
(without alignments)
301.263 Million cell updates/sec

Title: US-09-856-840C-2

Perfect score: 473

Sequence: 1 MFLVFLCCLHLVISHTPD.....VEWVYSTGQCRTICPTVG 81

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt_42.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Query Length	DB ID	Description
1	453	95.8	81	1	MCPI_H1RME
2	72	15.2	603	1	CEAI_MOUSE
3	71.5	15.1	407	1	YO14_CAEEL
4	71	15.0	1106	1	STC_DROME
5	68.5	14.5	4660	1	IRF2_RAT
6	68	14.4	159	1	KR93_HUMAN
7	68	14.4	288	1	SEY3_HUMAN
8	68	14.4	415	1	PIZ_MOUSE
9	68	14.4	441	1	YX17_SCHRO
10	68	14.4	813	1	YTOJ_CAEEL
11	68	14.4	1964	1	NTC4_MOUSE
12	68	14.4	3175	1	RFOA_DAV
13	67.5	14.3	1955	1	AGRI_CHICK
14	67.5	14.3	2321	1	NTC3_HUMAN
15	67	14.2	250	1	MSP2_HUMAN
16	66.5	14.1	159	1	KR98_HUMAN
17	66.5	14.1	1210	1	ATI9_MOUSE
					P81511 hirtudo medl
					O61129 mus musculu
					P34670 caenorhabd
					P40798 drosophila
					P98158 ratius novy
					O9byq3 homo sapien
					O43610 homo sapien
					P43252 mus musculu
					O9hdv3 schizosacch
					O19673 caenorhabd
					P31695 mus musculu
					P19811 equine arte
					P31696 gallus gall
					O9um47 homo sapien
					O76076 homo sapien
					O9byq6 homo sapien
					P59509 mus musculu

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OK protein - protein search, using sw model

Run on: April 29, 2004, 10:46:18 ; Search time 39 seconds
(without alignments)
655.307 Million cell updates/sec

Title: US-09-856-840C-2

Perfect score: 473
Sequence: 1 MFLVETCLHIVISHTPD.....VEMVETGQCRITPTVG 81

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1017041 segs, 315518202 residues
Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Query	Score	Match	Length	ID	Description
--------	-------	-------	-------	--------	----	-------------

1	81	17.1	340	5	P90627	P90627 leishmania
2	80	16.9	421	5	Q66JD6	Q66JD6 dictyostell
3	77	16.3	572	5	Q19594	Q19594 caenorhabdi
4	75.5	16.0	355	4	Q9H665	Q9H665 homo sapien
5	75.5	16.0	821	5	Q22631	Q22631 caenorhabdi
6	74	15.6	340	5	Q6WT30	Q6WT30 leishmania
7	74	15.6	340	5	Q9GQM5	Q9GQM5 leishmania
8	74	15.6	340	5	Q9GQN7	Q9GQN7 leishmania
9	72	15.2	335	5	Q9N6L3	Q9N6L3 caenorhabdi
10	72	15.2	1099	5	Q8IP49	Q8IP49 drosophila
11	72	15.2	1106	5	Q9Y025	Q9Y025 drosophila
12	71.5	15.1	340	5	Q25319	Q25319 leishmania
13	71	15.0	451	5	Q66K07	Q66K07 dictyostell
14	71	15.0	1069	5	Q9VBN2	Q9VBN2 drosophila
15	70	14.8	335	5	Q9NPF6	Q9NPF6 caenorhabdi
16	70	14.8	335	5	Q9NFW0	Q9NFW0 caenorhabdi
17	70	14.8	419	5	Q9NA38	Q9NA38 caenorhabdi
18	70	14.8	420	5	Q9NA61	Q9NA61 caenorhabdi
19	69	14.6	218	5	Q19618	Q19618 caenorhabdi
20	68.5	14.5	502	16	Q7UE37	Q7UE37 rhodospirill
21	68.5	14.5	765	5	Q9NLS0	Q9NLS0 sarcophaga
22	68	14.4	159	4	Q9BYQ3	Q9BYQ3 homo sapien
23	68	14.4	212	11	Q8CC99	Q8CC99 mus musculu
24	68	14.4	358	5	Q9U362	Q9U362 caenorhabdi
25	68	14.4	3175	12	Q91DM2	Q91DM2 equine arte
26	67.5	14.3	325	10	Q8LG72	Q8LG72 arabidopsis
27	67.5	14.3	869	13	Q42126	Q42126 xenopus lae
28	67.5	14.3	4007	4	Q86XX4	Q86XX4 homo sapien
29	67	14.2	241	5	Q45522	Q45522 caenorhabdi
30	67	14.2	355	13	Q802V2	Q802V2 brachydantio
31	67	14.2	400	12	Q81108	Q81108 heparitis b
32	67	14.2	527	5	P91835	P91835 caenorhabdi
33	67	14.2	649	6	Q28657	Q28657 oryctolagus
34	66.5	14.1	159	4	Q9BYQ0	Q9BYQ0 homo sapien
35	66.5	14.1	769	5	Q8MR15	Q8MR15 drosophila
36	66.5	14.1	1059	5	Q9W493	Q9W493 drosophila
37	66.5	14.1	1149	4	Q13577	Q13577 homo sapien
38	66.5	14.1	2026	4	Q00468	Q00468 homo sapien
39	66	14.0	847	13	Q90W12	Q90W12 oncorhynchus
40	66	14.0	1064	5	Q7YU01	Q7YU01 drosophila
41	65.5	13.8	324	10	Q9SM86	Q9SM86 oryza sativ
42	65.5	13.8	651	4	Q86U24	Q86U24 homo sapien
43	65.5	13.8	809	11	Q8CA82	Q8CA82 mus musculu
44	65.5	13.8	833	11	Q8K384	Q8K384 mus musculu
45	65.5	13.8	845	11	Q8BNJ2	Q8BNJ2 mus musculu

Search completed: April 29, 2004, 10:50:04
Job time : 41 secs

OM nucleic - nucleic search, using sw model

Run on: April 30, 2004, 06:56:35 ; Search time 2007 Seconds
(without alignments)
10042.108 Million cell updates/sec

Title: US-09-856-840C-1
Perfect score: 465
Sequence: 1 gacttggtaactcattcgat.....taaaaaaaaaaagaaaaa 465

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 segs, 2167516995 residues
Total number of hits satisfying chosen parameters: 6340544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: gb_da:*
2: gb_ntg:*
3: gb_in:*
4: gb_on:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vl:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_mu:*
21: em_or:*
22: em_ov:*
23: em_pac:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_sts:*

28: em_un:*
29: em_vl:*
30: em_htg_hum:*
31: em_htg_inv:*
32: em_htg_other:*
33: em_htg_mus:*
34: em_htg_pin:*
35: em_htg_rtd:*
36: em_htg_mam:*
37: em_htg_vrt:*
38: em_sy:*
39: em_hugo_hum:*
40: em_hugo_mus:*
41: em_hugo_other:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	Query	Match	Length	DB	ID	Description
No.							
1	465	100.0	465	3	HWE010948		AD10948 Hicudo me
2	465	100.0	465	6	AX026084		AX026084 Sequence
3	50.2	10.8	110000	3	AC116305_1		Continuation (2 of
4	49.8	10.7	182870	3	AC116960		AC116960 Dictyoste
5	49.2	10.6	6424	3	AC116924		AC116924 Dictyoste
6	49.2	10.6	110000	2	PFMAL13_17		Continuation (18 o
7	48.4	10.4	13138	3	AC116305_4		Continuation (5 of
8	48.4	10.4	110000	2	PFMAL8P1_01		Continuation (2 of
9	48.4	10.4	110000	3	AC116305_3		Continuation (4 of
10	48.4	10.4	302156	3	AC116977		AC116977 Dictyoste
11	48	10.3	110000	2	PFMAL6P1_12		Continuation (13 o
12	47.6	10.2	3016	3	DDU31631		U31631 Dictyostreil
13	47.6	10.2	169546	2	AC004157		AC004157 Plasmodiu
14	47.6	10.2	250707	3	AE014848		AE014848 Sequence
15	47.6	10.2	349954	6	AX196287		AX196287 Sequence
16	47.4	10.2	2523	9	BC038509		BC038509 Homo sapi
17	47.4	10.2	132254	3	AC116310		AC116310 Dictyoste
18	47.2	10.2	2917	9	BC054514		BC054514 Homo sapi
19	47.2	10.2	110000	3	AC116957_0		AC116957 Dictyoste
20	47.2	10.2	257109	3	AC115577		AC115577 Dictyoste
21	47	10.1	27684	8	HASMT		D31785 Pichia cana
22	47	10.1	125623	3	AC115599		AC115599 Dictyoste
23	46.8	10.1	57203	3	AC116989		AC116989 Dictyoste
24	46.6	10.0	31343	2	AC115576		AC115576 Dictyoste
25	46.6	10.0	31712	8	AP000415		AP000415 Arabidops
26	46.6	10.0	33270	3	AC116921		AC116921 Dictyoste
27	46.6	10.0	110000	2	PFMAL7P1_08		Continuation (9 of
28	46.6	10.0	117113	8	AC146575		AC146575 Medicago
29	46.6	10.0	234081	3	PFMAL4P2		AL035475 Plasmodiu
30	46.6	10.0	254733	3	AC117075		AC117075 Dictyoste
31	46.6	10.0	257109	3	AC115577		AC115577 Dictyoste
32	46.4	10.0	154071	3	AC115598		AC115598 Dictyoste
33	46.4	10.0	250195	3	AE014831		AE014831 Plasmodiu

Search completed: April 30, 2004, 09:28:17
Job time : 2012 secs

Querol, E., Reverter, D. and Vendrell, J.,
Inhibitor of metalocoxycyclopentadienes as fibrinolytic agent
Patent: WO 0031140-A 1 02-JUN-2000;
FRITZ HANS (DE); HORSTMANN JANNY (DE); LUDWIG MAXIMILIANS UNI
MÜNCHEN (DE); SOMMERHOF CHRISTIAN P (DE); AYLES FRANCESCO X (ES);
UNIV BARCELONA AUTONOMA (ES); CANALS FRANCESC (ES); QUEROL,
ENRIQUE (ES); REVERTER DAVID (ES); VENDRELL JOSEP (ES)

FEATURES	location/Qualifiers
source	1. .465

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/organism="Hirudo medicinalis"
/mol_type="unassigned DNA"
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22. .267

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/note="unnamed protein product; Product=I01"
/codon_start=1
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/db_xref="EEMREMBL:CAC09071"
/translation="MTLLFACGLHLYSSRRPDSSTLCQPDYQCFITRGAALPPLP
GGEONHPLPAWCEAGAEWMPVYSQACGCTTPIPIPV"

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ORIGIN

Query Match	100.0%;	Score 465;	DB 6;	Length 465;
Best Local Similarity	100.0%;	Pred. No. 9.9e-95;		
Matches 465;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy	1	GACTGGATACATCATGATCAATGTTCTCTGCTGTTCTGCTGCTGCTGCACTGGTG	60
Db	1	GACTGGATACATCATGATCAATGTTCTCTGCTGTTCTGCTGCTGCTGCACTGGTG	60
Qy	61	ATTGTGCGATACACCAAGTAGAGTTTCTTGTCTACCAACGACAGGTGTCTGT	120
Db	61	ATTGTGCGATACACCAAGTAGAGTTTCTTGTCTACCAACGACAGGTGTCTGT	120
Qy	121	TTGATTTGACAGAGAGGGGACCTTTGCTTCAGAGGGGAAATGCAATCCACTCTACA	180
Db	121	TTGATTTGACAGAGAGGGGACCTTTGCTTCAGAGGGGAAATGCAATCCACTCTACA	180
Qy	181	GCACCGTGTCGGCGGAAAGGGGCTGTAGAGTGGTCTCTACTACTACTGTCATGTGCG	240
Db	181	GCACCGTGTCGGCGGAAAGGGGCTGTAGAGTGGTCTCTACTACTACTGTCATGTGCG	240
Qy	241	ACACCTGCAATCCCATATGTGCAATGAATGACCCATGTGTCTACTAGGAGGCTTA	300
Db	241	ACACCTGCAATCCCATATGTGCAATGAATGACCCATGTGTCTACTAGGAGGCTTA	300
Qy	301	CTCCCATATTTTCCCTGAAGCATCTCTGTGGAATTTAAGGCAATTTCTCTCTGACT	360
Db	301	CTCCCATATTTTCCCTGAAGCATCTCTGTGGAATTTAAGGCAATTTCTCTCTGACT	360
Qy	361	AATTAATTTGCTGAGTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTTCTC	420
Db	361	AATTAATTTGCTGAGTTAAATTAATTAATTAATTAATTAATTAATTAATTAATTTCTC	420
Qy	421	GTTTGAAATAAATATGATGCAAGTAAAAAAGAAAAA 465	
Db	421	GTTTGAAATAAATATGATGCAAGTAAAAAAGAAAAA 465	

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OM nucleic - nucleic search, using sw model

Run on: April 30, 2004, 06:54:50 ; Search time 341 Seconds
(without alignments)
5792.997 Million cell updates/sec

Title: US-09-856-840C-1

Perfect score: 465

Sequence: 1 gacttgtaactcattcgat.....taaaaaaaaaaagaaaaa 465

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
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2: Geneseg1980s:*
3: Geneseg1990s:*
4: Geneseg2000s:*
5: Geneseg2001as:*
6: Geneseg2002as:*
7: Geneseg2003as:*
8: Geneseg2003bs:*
9: Geneseg2003cs:*
10: Geneseg2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	465	100.0	465	AA11268	AA11268 Hirudo me
2	47.6	10.2	110000	5 AA161373_2	Continuation (3 of
3	45	9.7	265	5 ABV07596	ABV07596 Human pro
4	45	9.7	887	3 AAC59297	AAC59297 Human sec
5	45	9.7	6071	6 AB132367	AB132367 Human imm
6	45	9.7	6071	6 AB134483	AB134483 Human imm
7	45	9.7	6071	6 AB170154	AB170154 Chemical1

ALIGNMENTS

RESULT 1	ID	AA11268	standard; cDNA; 465 BP.
XX	AC	AA11268;	
XX	DT	08-NOV-2000	(first entry)
DE	XX		
DE	XX		Hirudo medicinalis metalloproteinase inhibitor cDNA.
XX	XX		Recombinant, leech; metalloproteinase inhibitor; fibrin;
KW	KW		plasma carboxypeptidase B; fibrinolysis inhibitor; plasminogen;
KW	KW		blood clot; ds.
XX	XX		

C	8	44.8	9.6	337	7	ABX41811	ABX41811 Bovine ES
C	9	44.8	9.6	8779	6	AA61382	AA61382 Human gen
C	10	44.4	9.5	370	5	ABV07958	ABV07958 Human pro
C	11	44.4	9.5	19131	4	AA546716	AA546716 Tumour su
C	12	43.8	9.4	372	5	ABV37528	ABV37528 Human pro
C	13	43.8	9.4	5511	6	AB133871	AB133871 Human imm
C	14	43.8	9.4	110000	6	AB132787_1	Continuation (2 of
C	15	43.4	9.3	970	6	ABQ54211	ABQ54211 Human ova
C	16	43.4	9.3	1333	7	ACB96036	ACB96036 Trifolium
C	17	43.2	9.3	445	4	AA192310	AA192310 Human pol
C	18	43.2	9.3	3197	8	ACF05284	ACF05284 Plasmodiu
C	19	43.2	9.2	40862	6	AB134072	AB134072 Human imm
C	20	42.8	9.2	284	4	AAH70082	AAH70082 Human cer
C	21	42.8	9.2	289	2	AAV21217	AAV21217 Partial n
C	22	42.8	9.2	332	4	AAH70043	AAH70043 Human cer
C	23	42.8	9.2	473	8	ACH26237	ACH26237 Human adu
C	24	42.6	9.2	631	6	ABQ25138	ABQ25138 Oligonucle
C	25	42.6	9.2	631	6	ABQ25139	ABQ25139 Oligonucle
C	26	42.6	9.2	1781	9	ADBS8028	ADBS8028 Human gen
C	27	42.6	9.2	1781	9	ADBS8032	ADBS8032 Human gen
C	28	42.6	9.2	6731	6	ABK39963	ABK39963 Human che
C	29	42.6	9.2	8056	7	ABX42254	ABX42254 Haematopo
C	30	42.4	9.1	377	7	AAO11712	AAO11712 Bovine ES
C	31	42.4	9.1	3138	2	AAO11712	AAO11712 Shuttie v
C	32	42.4	9.1	3549	3	AA70223	AA70223 Plasmodiu
C	33	42.2	9.1	423	7	ABX38651	ABX38651 Bovine ES
C	34	42.2	9.1	464	4	AAH33241	AAH33241 Human col
C	35	42.2	9.1	1262	3	AACT9885	AACT9885 Human sec
C	36	42.2	9.1	10039	6	ABK70506	ABK70506 Human cDN
C	37	42.2	9.1	19124	2	AA172882	AA172882 Plasmodiu
C	38	42.2	9.1	19124	2	AA172882	AA172882 Plasmodiu
C	39	42.2	9.1	19124	3	AA298287	AA298287 Plasmodiu
C	40	42.2	9.0	843	5	ABV16074	ABV16074 Human pro
C	41	42.2	9.0	939	6	ABK33574	ABK33574 cDNA enco
C	42	42.2	9.0	939	7	ACB66879	ACB66879 cDNA enco
C	43	42.2	9.0	939	7	ACB66879	ACB66879 Novel hum
C	44	42.2	9.0	939	7	ACB66879	ACB66879 Novel hum
C	45	42.2	9.0	939	8	ABT44264	ABT44264 Human PRO

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OM nucleic - nucleic search, using sw model

Run on: April 30, 2004, 09:28:21 ; Search time 323 Seconds

(without alignments)
6512.108 Million cell updates/sec

Title: US-09-856-840C-1

Sequence: 1 gacttgtaaccatctgcgt.....taaaaaaaaaaaaaaa 465

Scoring table: IDENTITY_NUC

Gapop 10.0 ; Gapext 1.0

Searched: 2936184 seqs, 2261732022 residues

Total number of hits satisfying chosen parameters: 5872368

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Database: Published_Applications_NA.*

- Listing first 45 summaries
- 1: /cgn2_6/prodata/1/pubpna/US07_PUBCOMB.seq.*
 - 2: /cgn2_6/prodata/1/pubpna/US07_PUB_PUB.seq.*
 - 3: /cgn2_6/prodata/1/pubpna/US06_PUBCOMB.seq.*
 - 4: /cgn2_6/prodata/1/pubpna/US07_PUB_PUB.seq.*
 - 5: /cgn2_6/prodata/1/pubpna/US07_PUBCOMB.seq.*
 - 6: /cgn2_6/prodata/1/pubpna/US08_PUBCOMB.seq.*
 - 7: /cgn2_6/prodata/1/pubpna/US08_PUB_PUB.seq.*
 - 8: /cgn2_6/prodata/1/pubpna/US09_PUBCOMB.seq.*
 - 9: /cgn2_6/prodata/1/pubpna/US09_PUB_PUB.seq.*
 - 10: /cgn2_6/prodata/1/pubpna/US09_PUBCOMB.seq.*
 - 11: /cgn2_6/prodata/1/pubpna/US09_PUB_PUB.seq.*
 - 12: /cgn2_6/prodata/1/pubpna/US09_PUBCOMB.seq.*
 - 13: /cgn2_6/prodata/1/pubpna/US10_PUBCOMB.seq.*
 - 14: /cgn2_6/prodata/1/pubpna/US10_PUB_PUB.seq.*
 - 15: /cgn2_6/prodata/1/pubpna/US10_PUBCOMB.seq.*
 - 16: /cgn2_6/prodata/1/pubpna/US10_PUB_PUB.seq.*
 - 17: /cgn2_6/prodata/1/pubpna/US60_PUBCOMB.seq.*
 - 18: /cgn2_6/prodata/1/pubpna/US60_PUB_PUB.seq.*
 - 19: /cgn2_6/prodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result

Query

No.	Score	Match	Length	DB	ID	Description
1	47.6	10.2	513509	10	US-09-754-853A-4	Sequence 4, Appl.1
2	47	10.1	351	10	US-09-814-353-17579	Sequence 11579, A
3	46.8	10.1	620	13	US-10-424-599-71272	Sequence 71272, A
4	46.2	9.9	783	13	US-10-424-599-142220	Sequence 2, Appl.1
5	45.8	9.8	695	12	US-10-401-038-2	Sequence 340, Appl
6	45	9.7	6071	15	US-10-311-455-340	Sequence 36, Appl
7	45	9.7	6071	15	US-10-240-485-36	Sequence 6976, Ap
8	44.8	9.6	337	9	US-09-960-352-6976	Sequence 123899, A
9	44.8	9.6	1413	13	US-10-424-599-112225	Sequence 112225, A
10	44.8	9.6	1413	13	US-10-424-599-112225	Sequence 345, App
11	44.8	9.6	8779	13	US-10-312-841-1	Sequence 5335, App
12	44.8	9.6	3673778	15	US-10-312-841-1	Sequence 11622, A
13	44.4	9.5	302	10	US-09-814-353-535	Sequence 441, App
14	44.4	9.5	302	10	US-09-814-353-11622	Sequence 18599, A
15	44.4	9.5	19131	13	US-10-221-714A-441	Sequence 890, App
16	44.2	9.5	461	10	US-09-814-353-18599	Sequence 135986, A
17	44	9.5	466	13	US-10-424-599-135986	Sequence 13378, A
18	43.8	9.4	577	13	US-10-424-599-13378	Sequence 1644, Ap
19	43.8	9.4	655	13	US-10-424-599-13378	Sequence 1, Appl.1
20	43.8	9.4	5511	15	US-10-311-455-1844	Sequence 1, Appl.1
21	43.8	9.4	640681	9	US-09-790-968-1	Sequence 1, Appl.1
22	43.4	9.3	970	16	US-10-264-049-91	Sequence 1, Appl.1
23	43.4	9.3	3673778	15	US-10-312-841-1	Sequence 36762, A
24	43.2	9.3	222	13	US-10-424-599-36762	Sequence 65293, A
25	43.2	9.3	1358	13	US-10-424-599-65293	Sequence 4900, Ap
26	43.2	9.3	3673778	15	US-10-312-841-1	Sequence 11195, A
27	43	9.2	406	10	US-09-814-353-4900	Sequence 2035, Ap
28	43	9.2	406	10	US-09-814-353-11195	Sequence 8381, Ap
29	43	9.2	708	10	US-09-814-353-8381	Sequence 2045, Ap
30	43	9.2	708	10	US-09-814-353-2045	Sequence 5567, Ap
31	43	9.2	40862	15	US-10-311-455-2045	Sequence 11854, A
32	42.8	9.2	337	10	US-09-814-353-5567	Sequence 13449, A
33	42.8	9.2	337	10	US-09-814-353-11854	Sequence 5894, Ap
34	42.8	9.2	473	10	US-09-918-955-13449	Sequence 12175, A
35	42.8	9.2	746	10	US-09-814-353-5894	Sequence 100865, A
36	42.8	9.2	746	10	US-09-814-353-12175	Sequence 18240, Ap
37	42.8	9.2	1061	13	US-10-424-599-100865	Sequence 3227, A
38	42.6	9.2	350	10	US-09-814-353-18240	Sequence 9552, Ap
39	42.6	9.2	440	10	US-09-814-353-3227	Sequence 5567, Ap
40	42.6	9.2	440	10	US-09-814-353-9552	Sequence 11856, A
41	42.6	9.2	579	10	US-09-814-353-5569	Sequence 7419, Ap
42	42.6	9.2	579	10	US-09-814-353-11856	Sequence 106126, A
43	42.6	9.2	6751	17	US-10-251-166-44	
44	42.4	9.1	377	9	US-09-960-352-7419	
45	42.4	9.1	515	13	US-10-424-599-106126	

Search completed: April 30, 2004, 11:15:23
Job time : 333 secs

OM nucleic - nucleic search, using sw model

Run on: April 30, 2004, 07:51:05 : Search time 2507 Seconds
(without alignments)
5538.857 Million cell updates/sec

Title: US-09-856-840C-1

Perfect score: 465
Sequence: 1 gacttgtaactcctcgcgt.....taaaaaaaaaaagaaaaa 465

Scoring table: IDENTITY NUC
Gapop 10.0, Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: em_estda:*
2: em_esthum:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hlc:*
9: gb_est1:*
10: gb_est2:*
11: gb_hlc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_hiv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rtd:*
26: em_gss_prg:*
27: em_gss_vrt1:*

28: gb_gss1:*
29: gb_gss2:*
Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	59	12.7	452	13	BX446269
2	56.8	12.2	1201	13	BX446296
3	54.8	11.8	1162	9	AL513719
4	53	11.4	937	29	CNS0060XP
5	52.8	11.4	1201	13	BX446296
6	52.6	11.3	1045	29	CNS03YEA
7	52.4	11.3	427	13	BX403499
8	52	11.2	776	29	CNS01268
9	51.8	11.1	970	29	CNS0162E
10	51.6	11.1	179	9	AL275113
11	51.4	11.1	1121	13	BX38325
12	51.2	11.0	316	14	CF545414
13	51.2	11.0	386	13	C90680
14	51.2	11.0	392	13	BX424882
15	51.2	11.0	1201	13	BX403761
16	51	11.0	1104	9	AL513809
17	50.8	10.9	392	13	BX424882
18	50.8	10.9	1201	9	AL513975
19	50.8	10.9	1201	9	AL513975
20	50.4	10.8	425	14	CF980658
21	50.4	10.8	441	14	CF980752
22	50.2	10.8	469	13	BX425137
23	50.2	10.8	908	13	BX429815
24	50.2	10.8	970	29	CNS0182E
25	50.2	10.8	1201	13	BX356198
26	50	10.8	501	14	CF302974
27	50	10.8	1162	9	AL513719
28	49.8	10.7	381	13	BX425197
29	49.8	10.7	1201	13	BX458623
30	49.6	10.7	243	14	CF383661
31	49.6	10.7	506	9	AL514791
32	49.6	10.7	994	29	CNS04NOJ
33	49	10.5	173	12	BJ423644
34	49	10.5	248	14	CF383673
35	48.8	10.5	274	13	BX446690
36	48.8	10.5	356	13	BX446758
37	48.8	10.5	625	29	CNS036A2
38	48.8	10.5	658	29	CNS03WK1
39	48.8	10.5	911	13	BX446782
40	48.6	10.5	240	9	AU073206
41	48.6	10.5	264	14	CF622488
42	48.6	10.5	324	14	CF545077
43	48.6	10.5	583	29	CNS0440G
44	48.6	10.5	716	13	C22772

45 48.6 10.5 780 13 E0843635
Search completed: April 30, 2004, 10:10:17
Job time : 2511 secs

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